



SEQUENCE LISTING

Selden, Richard F.
Miller, Allan M.
Treco, Douglas A.

<120> OPTIMIZED MESSENGER RNA

<130> 10278-009001

<140> US 09/407,605

<141> 1999-09-28

<150> US 60/130,241

<151> 1999-04-20

<150> 60/102,239

<151> 1998-09-29

<160> 136

<170> FastSEQ for Windows Version 4.0

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<213> Artificial Sequence

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Cys	Leu	Leu	Arg	Phe	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	
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gcc	gtg	gag	ctg	agc	tgg	gac	tac	atg	cag	agc	gac	ctg	ggc	gag	ctg	147
Ala	Val	Glu	Leu	Ser	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	
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Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	
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aac	acc	agc	gtg	gtg	tac	aag	aag	acc	ctg	ttc	gtg	gag	ttc	acc	gac	243
Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	
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cac	ctg	ttc	aac	atc	gcc	aag	ccc	cgc	ccc	ccc	tgg	atg	ggc	ctg	ctg	291
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His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu	
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ggc ccc acc atc cag gcc gag gtg tac gac acc gtg gtg atc acc ctg	339
Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu	
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aag aac atg gcc agc cac ccc gtg agc ctg cac gcc gtg ggc gtg agc	387
Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser	
110 115 120	
tac tgg aag gcc agc gag ggc gcc gag tac gac gac cag acc agc cag	435
Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln	
125 130 135	
cgc gag aag gag gac gac aag gtg ttc ccc ggc ggc agc cac acc tac	483
Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr	
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gtg tgg cag gtg ctg aag gag aac ggc ccc atg gcc agc gac ccc ctg	531
Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu	
160 165 170	
tgc ctg acc tac agc tac ctg agc cac gtg gac ctg gtg aag gac ctg	579
Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu	
175 180 185	
aac agc ggc ctg atc ggc gcc ctg ctg gtg tgc cgc gag ggc agc ctg	627
Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu	
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gcc aag gag aag acc cag acc ctg cac aag ttc atc ctg ctg ttc gcc	675
Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala	
205 210 215	
gtg ttc gac gag ggc aag agc tgg cac agc gag acc aag aac agc ctg	723
Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu	
220 225 230 235	
atg cag gac cgc gac gcc gcc agc gcc cgc gcc tgg ccc aag atg cac	771
Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His	
240 245 250	
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Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys	
255 260 265	
cac cgc aag agc gtg tac tgg cac gtg atc ggc atg ggc acc acc ccc	867
His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro	
270 275 280	
gag gtg cac agc atc ttc ctg gag ggc cac acc ttc ctg gtg cgc aac	915
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn	
285 290 295	
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His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala	

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Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile				
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agc agc cac cag cac gac ggc atg gag gcc tac gtg aag gtg gac agc				1059
Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser				
335		340	345	
tgc ccc gag gag ccc cag ctg cgc atg aag aac aac gag gag gcc gag				1107
Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu				
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Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe				
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Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys				
380		385	390	395
aag cac ccc aag acc tgg gtg cac tac atc gcc gcc gag gag gag gac				1251
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp				
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tgg gac tac gcc ccc ctg gtg ctg gcc ccc gac gac cgc agc tac aag				1299
Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys				
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Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys				
430		435	440	
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Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu				
460		465	470	475
gtg ggc gac acc ctg ctg atc atc ttc aag aac cag gcc agc cgc ccc				1491
Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro				
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Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser				
495		500	505	
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Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu				
510		515	520	
ccc ggc gag atc ttc aag tac aag tgg acc gtg acc gtg gag gac ggc				1635
Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly				
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Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp	
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acc atc agc gtg gag atg aag aag gag gac ttc gac atc tac gac gag	2403
Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu	
780 785 790 795	
gac gag aac cag agc ccc cgc agc ttc cag aag aag acc cgc cac tac	2451
Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr	
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Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser	
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ccc cac gtg ctg cgc aac cgc gcc cag agc ggc agc gtg ccc cag ttc	2547
Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe	
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Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro	
845 850 855	
ctg tac cgc ggc gag ctg aac gag cac ctg ggc ctg ctg ggc ccc tac	2643
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr	
860 865 870 875	
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Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln	
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Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu	
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Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn	
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gag acc aag acc tac ttc tgg aag gtg cag cac cac atg gcc ccc acc	2835
Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr	
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Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp	
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Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys	
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His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln	
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atg gag gac ccc acc ttc aag gag aac tac cgc ttc cac gcc atc aac	3123
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ggc tac atc atg gag acc ctg aaa ggc ctg gtg atg gcc cag gac cag	3171
Gly Tyr Ile Met Asp Thr Leu Lys Gly Leu Val Met Ala Gln Asp Gln	
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Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val	
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gag atg ctg ccc agc aag gcc ggc atc tgg cgc gtg gag tgc ctg atc	3363
Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile	
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Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser	
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aac aag tgc cag acc ccc ctg ggc atg gcc agc ggc cac atc cgc gac	3459
Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp	
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ttc cag atc acc gcc agc ggc cag tac ggc cag tgg gcc ccc aag ctg	3507
Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu	
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Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu	
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ccc ttc agc tgg atc aag gtg gac ctg ctg gcc ccc atg atc atc cac	3603
Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His	
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Gly Ile Lys Thr Gln Gly Ala Arg Gln Asn Phe Ser Ser Leu Tyr Ile	
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Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr	

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Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val			
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gac agc agc ggc atc aag cac aac atc ttc aac ccc ccc atc atc gcc			3795
Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala			
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Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu			
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cgc atg gag ctg atg ggc tgc gac ctg aac agc tgc agc atg ccc ctg			3891
Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu			
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Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser			
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Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly			
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gtg acc acc cag ggc gtg aag agc ctg ctg acc agc atg tac gtg aag			4131
Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys			
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Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe			
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ttc cag aac ggc aag gtg aag gtg ttc cag ggc aac cag gac agc ttc			4227
Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe			
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Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu			
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Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu			
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4376

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Cys	Leu	Leu	Arg	Phe	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	
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			30				35					40				

ccc	gtg	gac	gcc	cgc	ttc	ccc	ccc	cgc	gtg	ccc	aag	agc	ttc	ccc	ttc	195
Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	
		45				50					55					

aac	acc	agc	gtg	gtg	tac	aag	aag	acc	ctg	ttc	gtg	gag	ttc	acc	gac	243
Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	
	60				65				70					75		

cac	ctg	ttc	aac	atc	gcc	aag	ccc	cgc	ccc	ccc	tgg	atg	ggc	ctg	ctg	291
His	Leu	Phe	Asn	Ile	Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	
			80					85						90		

ggc	ccc	acc	atc	cag	gcc	gag	gtg	tac	gac	acc	gtg	gtg	atc	acc	ctg	339
Gly	Pro	Thr	Ile	Gln	Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	
			95				100						105			

aag	aac	atg	gcc	agc	cac	ccc	gtg	agc	ctg	cac	gcc	gtg	ggc	gtg	agc	387
Lys	Asn	Met	Ala	Ser	His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	
		110					115					120				

tac	tgg	aag	gcc	agc	gag	ggc	gcc	gag	tac	gac	gac	cag	acc	agc	cag	435
Tyr	Trp	Lys	Ala	Ser	Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	
	125					130				135						

cgc	gag	aag	gag	gac	gac	aag	gtg	ttc	ccc	ggc	ggc	agc	cac	acc	tac	483
Arg	Glu	Lys	Glu	Asp	Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	
	140					145				150					155	

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Val	Trp	Gln	Val	Leu	Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	

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Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu			
175	180	185	
aac agc ggc ctg atc ggc gcc ctg ctg gtg tgc cgc gag ggc agc ctg			627
Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu			
190	195	200	
gcc aag gag aag acc cag acc ctg cac aag ttc atc ctg ctg ttc gcc			675
Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala			
205	210	215	
gtg ttc gac gag ggc aag agc tgg cac agc gag acc aag aac agc ctg			723
Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu			
220	225	230	235
atg cag gac cgc gac gcc gcc agc gcc cgc gcc tgg ccc aag atg cac			771
Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His			
240	245	250	
acc gtg aac ggc tac gtg aac cgc agc ctg ccc ggc ctg atc ggc tgc			819
Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys			
255	260	265	
cac cgc aag agc gtg tac tgg cac gtg atc ggc atg ggc acc acc ccc			867
His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro			
270	275	280	
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Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn			
285	290	295	
cac cgc cag gcc agc ctg gag atc agc ccc atc acc ttc ctg acc gcc			963
His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala			
300	305	310	315
cag acc ctg ctg atg gac ctg ggc cag ttc ctg ctg ttc tgc cac atc			1011
Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile			
320	325	330	
agc agc cac cag cac gac ggc atg gag gcc tac gtg aag gtg gac agc			1059
Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser			
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tgc ccc gag gag ccc cag ctg cgc atg aag aac aac gag gag gcc gag			1107
Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu			
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gac tac gac gac gac ctg acc gac agc gag atg gac gtg gtg cgc ttc			1155
Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe			
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gac gac gac aac agc ccc agc ttc atc cag atc cgc agc gtg gcc aag			1203
Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys			
380	385	390	395

aag cag ggg aag acc tgg gtg cac tac atc gcc gcc gag gag gag gac	1251
Lys Gln Gly Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp	
400 405 410	
tgg gac tac gcc ccc ctg gtg ctg gcc ccc gac gac cgc agc tac aag	1299
Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys	
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Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys	
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Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu	
445 450 455	
gcc atc cag cac gag agc ggc atc ctg ggc ccc ctg ctg tac ggc gag	1443
Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu	
460 465 470 475	
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Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro	
480 485 490	
tac aac atc tac ccc cac ggc atc acc gac gtg cgc ccc ctg tac agc	1539
Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser	
495 500 505	
cgc cgc ctg ccc aag ggc gtg aag cac ctg aag gac ttc ccc atc ctg	1587
Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu	
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Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly	
525 530 535	
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Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe	
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Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu	
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Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser	
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Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser	
590 595 600	
tgg tac ctg acc gag aac atc cag cgc ttc ctg ccc aac ccc gcc ggc	1875
Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly	
605 610 615	

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ctg agc gtg ttc ttc agc ggc tac acc ttc aag cac aag atg gtg tac Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr 670 675 680	2067
gag gac acc ctg acc ctg ttc ccc ttc agc ggc gag acc gtg ttc atg Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met 685 690 695	2115
agc atg gag aac ccc ggc ctg tgg atc ctg ggc tgc cac aac agc gac Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp 700 705 710 715	2163
ttc cgc aac cgc ggc atg acc gcc ctg ctg aag gtg agc agc tgc gac Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp 720 725 730	2211
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tac ctg ctg agc aag aac aac gcc atc gag ccc cgc agg cgc agg cgc Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Arg Arg Arg Arg 750 755 760	2307
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gac gag gac gag aac cag agc ccc cgc agc ttc cag aag aag acc cgc Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg 800 805 810	2451
cac tac ttc atc gcc gcc gtg gag cgc ctg tgg gac tac ggc atg agc His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser 815 820 825	2499
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Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr	
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Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly	
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ccc tac atc cgc gcc gag gtg gag gac aac atc atg gtg acc ttc cgc	2691
Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg	
880 885 890	
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Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr	
895 900 905	
gag gag gac cag cgc cag ggc gcc gag ccc cgc aag aac ttc gtg aag	2787
Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys	
910 915 920	
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Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala	
925 930 935	
ccc acc aag gac gag ttc gac tgc aag gcc tgg gcc tac ttc agc gac	2883
Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp	
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Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu	
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Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr	
975 980 985	
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Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser	
990 995 1000	
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Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn	
1005 1010 1015	
atc cag atg gag gac ccc acc ttc aag gag aac tac cgc ttc cac gcc	3123
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala	
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Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln	
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Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn	
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Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys	

1070	1075	1080	
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acc gtg gag atg ctg ccc agc aag gcc ggc atc tgg cgc gtg gag tgc Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys 1100	1105	1110 1115	3363
ctg atc ggc gag cac ctg cac gcc ggc atg agc acc ctg ttc ctg gtg Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val 1120	1125	1130	3411
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acc ctg cgc atg gag ctg atg ggc tgc gac ctg aac agc tgc agc atg Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met 1280	1285	1290	3891
ccc ctg ggc atg gag agc aag gcc atc agc gac gcc cag atc acc gcc Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala 1295	1300	1305	3939

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 Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
 1310 1315 1320

cgc ctg cac ctg cag ggc cgc agc aac gcc tgg cgc ccc cag gtg aac 4035
 Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn
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aac ccc aag gag tgg ctg cag gtg gac ttc cag aag acc atg aag gtg 4083
 Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
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 1375 1380 1385

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 Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
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 Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg
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 Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
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 Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
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 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 35 40 45
 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 50 55 60
 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile

65					70					75					80
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
				85					90					95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
			100					105					110		
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
		115					120					125			
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
	130					135					140				
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
145					150					155					160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
			165						170					175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile
			180					185					190		
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr
	195						200					205			
Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly
	210					215					220				
Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp
225					230					235					240
Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr
				245					250					255	
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val
			260					265					270		
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile
	275						280					285			
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser
	290					295				300					
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met
305					310					315					320
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His
				325					330					335	
Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro
		340						345					350		
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp
	355						360					365			
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser
	370					375					380				
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr
385					390					395					400
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro
				405					410					415	
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn
			420					425					430		
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met
	435					440						445			
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu
	450					455				460					
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu
465					470					475					480
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro
				485					490					495	
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys
		500						505					510		
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe
		515					520					525			

Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	530	535	540
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	545	550	555
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	565	570	575
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	580	585	590
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	595	600	605
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	610	615	620
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	625	630	635
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	645	650	655
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	660	665	670
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	675	680	685
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	690	695	700
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	705	710	715
Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	725	730	735
Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	740	745	750
Asn	Asn	Ala	Ile	Glu	Pro	Arg	Leu	Glu	Glu	Ile	Thr	Arg	Thr	Thr	Leu	755	760	765
Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	770	775	780
Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	785	790	795
Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	805	810	815
Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	820	825	830
Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	835	840	845
Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	850	855	860
Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	865	870	875
Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	885	890	895
Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	900	905	910
Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	915	920	925
Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	930	935	940
Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	945	950	955
His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	965	970	975
Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe			

	980		985		990
Phe Thr Ile	Phe Asp Glu Thr Lys Ser Trp Tyr	Phe Thr Glu Asn Met			
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Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met	Glu Asp Pro Thr				
1010	1015	1020			
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp					
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Thr Leu Lys Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr					
	1045	1050		1055	
Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser					
	1060	1065		1070	
Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu					
	1075	1080		1085	
Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser					
	1090	1095		1100	
Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His					
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Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr					
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Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala					
	1140	1145		1150	
Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr					
	1155	1160		1165	
Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile					
	1170	1175		1180	
Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln					
1185	1190	1195		1200	
Gly Ala Arg Gln Asn Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile					
	1205	1210		1215	
Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser					
	1220	1225		1230	
Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile					
	1235	1240		1245	
Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu					
	1250	1255		1260	
His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met					
1265	1270	1275		1280	
Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys					
	1285	1290		1295	
Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met					
	1300	1305		1310	
Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg					
	1315	1320		1325	
Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln					
	1330	1335		1340	
Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly					
1345	1350	1355		1360	
Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser					
	1365	1370		1375	
Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys					
	1380	1385		1390	
Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn					
	1395	1400		1405	
Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln					
	1410	1415		1420	
Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu					
1425	1430	1435		1440	

Ala Gln Asp Leu Tyr
1445

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<211> 1447

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 4

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Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser
			20					25					30		
Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg
		35					40					45			
Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val
	50					55					60				
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile
65					70					75				80	
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
				85					90					95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
			100					105					110		
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
		115					120					125			
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
	130					135					140				
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
145					150					155				160	
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
				165				170						175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile
			180					185					190		
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr
		195					200					205			
Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly
	210					215					220				
Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp
225					230					235				240	
Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr
				245					250					255	
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val
			260					265					270		
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile
		275				280						285			
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser
	290					295					300				
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met
305					310					315				320	
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His
				325					330					335	
Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro
			340					345					350		
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp

		355						360					365				
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser		
	370					375					380						
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	Gln	Gly	Lys	Thr		
385					390					395					400		
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro		
				405					410					415			
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn		
			420					425					430				
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met		
		435					440					445					
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu		
		450				455					460						
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu		
465					470					475					480		
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro		
				485					490					495			
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys		
			500					505					510				
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe		
		515					520					525					
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp		
		530				535					540						
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg		
545					550					555					560		
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu		
				565					570					575			
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val		
			580					585					590				
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu		
		595					600					605					
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp		
		610				615					620						
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val		
625					630					635					640		
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp		
				645					650					655			
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe		
			660					665					670				
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr		
		675					680					685					
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro		
		690				695					700						
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly		
705					710					715							

Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	820	825	830
Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	835	840	845
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	850	855	860
Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	865	870	875
Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	885	890	895
Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	900	905	910
Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	915	920	925
Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	930	935	940
Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	945	950	955
Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	965	970	975
Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	980	985	990
Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	995	1000	1005
Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	1010	1015	1020
Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	1025	1030	1035
Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	1045	1050	1055
Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	1060	1065	1070
Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	1075	1080	1085
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	1090	1095	1100
Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	1105	1110	1115
Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	1125	1130	1135
Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	1140	1145	1150
Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	1155	1160	1165
His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser	1170	1175	1180
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys	1185	1190	1195
Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	1205	1210	1215
Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	1220	1225	1230
Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	1235	1240	1245
Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	1250	1255	1260
Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu			

1265 1270 1275 1280
 Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu
 1285 1290 1295
 Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr
 1300 1305 1310
 Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln
 1315 1320 1325
 Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp
 1330 1335 1340
 Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr
 1345 1350 1355 1360
 Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu
 1365 1370 1375
 Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn
 1380 1385 1390
 Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val
 1395 1400 1405
 Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 1410 1415 1420
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly
 1425 1430 1435 1440
 Cys Glu Ala Gln Asp Leu Tyr
 1445

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<220>
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<221> misc_feature
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 <223> n = a, g, c, or t

<400> 5
 gaggagnnnn nnnnnn

16

<210> 6
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<220>
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<221> misc_feature
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16

<210> 7
 <211> 118
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<213> Homo sapiens

<400> 7

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<210> 8

<211> 104

<212> DNA

<213> Homo sapiens

<400> 8

gactacatgc agagcgacct gggcgagctg cccgtggacg cccgcttccc cccccgcgtg 60
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<210> 9

<211> 88

<212> DNA

<213> Homo sapiens

<400> 9

cctgttcgtg gagttcacccg accacctgtt caacatcgcc aagccccgcc cccctggat 60
gggcctgctg ggccccctaca agctttac 88

<210> 10

<211> 119

<212> DNA

<213> Homo sapiens

<400> 10

gtaaagcttg taggggcca gcaggcccat ccaggggggg cggggcttgg cgatgttgaa 60
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<210> 11

<211> 107

<212> DNA

<213> Homo sapiens

<400> 11

ggaagctctt gggcacgcgg ggggggaagc gggcgctccac gggcagctcg cccaggctcg 60
tctgcatgta gtcccagctc agctccacgg cgcccaggta gtagcgg 107

<210> 12

<211> 84

<212> DNA

<213> Homo sapiens

<400> 12

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tgcatgctag cctacgaatt ctac 84

<210> 13

<211> 115

<212> DNA

<213> Homo sapiens

<400> 13

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<210> 14
<211> 103
<212> DNA
<213> Homo sapiens

<400> 14
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caaggtgttc cccggcgga gccacaccta cgtgtggcag gtg 103

<210> 15
<211> 79
<212> DNA
<213> Homo sapiens

<400> 15
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cacgtgctac aagctttac 79

<210> 16
<211> 107
<212> DNA
<213> Homo sapiens

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<210> 17
<211> 101
<212> DNA
<213> Homo sapiens

<400> 17
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ccctcgctgg ccttcagta gctcacgccc acggcgtgca g 101

<210> 18
<211> 89
<212> DNA
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<210> 19
<211> 122
<212> DNA
<213> Homo sapiens

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<210> 20
 <211> 110
 <212> DNA
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<400> 20
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<210> 21
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 21
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<210> 22
 <211> 108
 <212> DNA
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<400> 22
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 <212> DNA
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<400> 23
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<210> 24
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<210> 25
 <211> 99
 <212> DNA
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<400> 25
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<210> 26
 <211> 100

<212> DNA
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<400> 26
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<210> 27
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 27
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<210> 28
 <211> 84
 <212> DNA
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<400> 28
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 ctctacggat cctacaagct ttac 84

<210> 29
 <211> 109
 <212> DNA
 <213> Homo sapiens

<400> 29
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<210> 30
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 30
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 aggccctccat gccgtcgtgc tgggtggctgc tgatgtggca g 101

<210> 31
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 31
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<210> 32
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 32
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 tacgaattct ac 72

<210> 33
 <211> 122
 <212> DNA
 <213> Homo sapiens

<400> 33
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 ag 122

<210> 34
 <211> 120
 <212> DNA
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<400> 34
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 <211> 115
 <212> DNA
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<400> 35
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<210> 36
 <211> 86
 <212> DNA
 <213> Homo sapiens

<400> 36
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 cccggcgaga tctctacaag ctttac 86

<210> 37
 <211> 109
 <212> DNA
 <213> Homo sapiens

<400> 37
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 ttgggcaggc ggccgctgta cagggggcgc acgtcggtga tgccgtggg 109

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 <211> 114
 <212> DNA
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<400> 38
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<210> 39
 <211> 121
 <212> DNA
 <213> Homo sapiens

<400> 39
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 c 121

<210> 40
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 40
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<210> 41
 <211> 102
 <212> DNA
 <213> Homo sapiens

<400> 41
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 aagagcgacc ccgctgcct gaccgctac tacagcagct tc 102

<210> 42
 <211> 103
 <212> DNA
 <213> Homo sapiens

<400> 42
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 gagagcgtgg accagcgcgg caaccagatc atgagcgaca agc 103

<210> 43
 <211> 61
 <212> DNA
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<400> 43
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 c 61

<210> 44
 <211> 87
 <212> DNA
 <213> Homo sapiens

<400> 44
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 cgcttgctgc tcatgatctg gttgccg 87

<210> 45
 <211> 101
 <212> DNA
 <213> Homo sapiens

<400> 45
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 tcgcgctcca tgttcacgaa gctgctgtag tagcgggtca g 101

<210> 46
 <211> 78
 <212> DNA
 <213> Homo sapiens

<400> 46
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 gatctctacg aattctac 78

<210> 47
 <211> 120
 <212> DNA
 <213> Homo sapiens

<400> 47
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<210> 48
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 <212> DNA
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<400> 48
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 aagatg 126

<210> 49
 <211> 95
 <212> DNA
 <213> Homo sapiens

<400> 49
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 gagaaccccg gcctgtggat ccctacaagc ttac 95

<210> 50
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 50
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 ctgaagggga acagggtcag ggtgtcctcg tacaccatct tgtgcttgaa ggtgtagcc 119

<210> 51
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<212> DNA

<213> Homo sapiens

<400> 51

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cacctcgtgc aggcacacgc tcagctgcag gctgtcgaac acgtagccgt tgatgctgtg	120
catg	124

<210> 52

<211> 98

<212> DNA

<213> Homo sapiens

<400> 52

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cgctggatgt tctcggtcag gtaccctacg aattctac	98

<210> 53

<211> 111

<212> DNA

<213> Homo sapiens

<400> 53

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<210> 54

<211> 102

<212> DNA

<213> Homo sapiens

<400> 54

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<210> 55

<211> 105

<212> DNA

<213> Homo sapiens

<400> 55

gagatcgact acgacgacac catcagcgtg gagatgaaga aggaggactt cgacatctac	60
gacgaggacg agaaccagag cccccgcagc ttccagaaga agacc	105

<210> 56

<211> 79

<212> DNA

<213> Homo sapiens

<400> 56

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cacgtgctac aagctttac	79

<210> 57

<211> 101

<212> DNA

<213> Homo sapiens

<400> 57
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 <212> DNA
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<400> 58
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 atgggtgtcgt cgtagtcgat ctctctctgg tcgctctgca gggtg 105

<210> 59
 <211> 108
 <212> DNA
 <213> Homo sapiens

<400> 59
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 ctgatgtcct cgtagctgtc ctcgtagtag tcgccggtgt tcttgctg 108

<210> 60
 <211> 83
 <212> DNA
 <213> Homo sapiens

<400> 60
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 cccaggatcc ctacgaattc tac 83

<210> 61
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 <212> DNA
 <213> Homo sapiens

<400> 61
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 gaaggtgggtg ttccaggagt tcaccgacgg cagcttcacc cagccctgt accgc 115

<210> 62
 <211> 111
 <212> DNA
 <213> Homo sapiens

<400> 62
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 aacatcatgg tgaccgtgca ggagttcgcc ctgttcttca ccattcttga c 111

<210> 63
 <211> 106
 <212> DNA
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<400> 63
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atccagatgg aggacccac cttcaaggag aactaccgct tccacg 106

<210> 64
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 64
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 tccgctggta ccctacaagc ttac 85

<210> 65
 <211> 115
 <212> DNA
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<400> 65
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 gtgtccatga tgtagccgtt gatggcgtgg aagcggtagt tctccttgaa ggtgg 115

<210> 66
 <211> 99
 <212> DNA
 <213> Homo sapiens

<400> 66
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 accagctctt ggtctcgtcg aagatgggtga agaacaggg 99

<210> 67
 <211> 110
 <212> DNA
 <213> Homo sapiens

<400> 67
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 gcaggcccag gtgctcgttc agctcgccgc ggtacagggg ctgggtgaag 110

<210> 68
 <211> 93
 <212> DNA
 <213> Homo sapiens

<400> 68
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 gcgcggttgc gcagcacgtg ctacgaattc tac 93

<210> 69
 <211> 116
 <212> DNA
 <213> Homo sapiens

<400> 69
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<210> 70

<211> 120
 <212> DNA
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<400> 70
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 aaggacgagt tcgactgcaa ggcctggggc tacttcagcg acgtggacct ggagaaggac 120

<210> 71
 <211> 91
 <212> DNA
 <213> Homo sapiens

<400> 71
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 cacggcggcc aggtgaccct acaagcttta c 91

<210> 72
 <211> 113
 <212> DNA
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<400> 72
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<210> 73
 <211> 121
 <212> DNA
 <213> Homo sapiens

<400> 73
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 acctccaga agtaggtctt ggtctcgttg ggcttcacga agttcttgcg gggctcggcg 120
 c 121

<210> 74
 <211> 93
 <212> DNA
 <213> Homo sapiens

<400> 74
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 cctggttgcg gaaggtcacc ctacgaattc tac 93

<210> 75
 <211> 120
 <212> DNA
 <213> Homo sapiens

<400> 75
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 ttcagcggcc acgtgttcac cgtgcgcaag aaggaggagt acaagatggc cctgtacaac 120

<210> 76
 <211> 122
 <212> DNA

<213> Homo sapiens

<400> 76

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gtggagtgcc tgatcggcga gcacctgcac gccggcatga gcaccctgtt cctgggtgtac	120
ag	122

<210> 77

<211> 102

<212> DNA

<213> Homo sapiens

<400> 77

caacaagtgc cagaccccc tgggcatggc cagcggccac atccggcact tccagatcac	60
cgccagcggc cagtacggcc agtgggcccc tacaagcttt ac	102

<210> 78

<211> 123

<212> DNA

<213> Homo sapiens

<400> 78

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atgtggccgc tggccatgcc cagggggggtc tggcacttgt tgctgtacac caggaacagg	120
gtg	123

<210> 79

<211> 125

<212> DNA

<213> Homo sapiens

<400> 79

ctcatgccgg cgtgcagggtg ctgcccgatc aggcactcca cgcgccagat gccggccttg	60
ctgggcagca tctccacggg ctggaacacg cgggggtaca ggttgtacag ggccatcttg	120
tactc	125

<210> 80

<211> 96

<212> DNA

<213> Homo sapiens

<400> 80

ctccttcttg cgcacgggtga acacgtggcc gctgaagtgg atgctgtgga tgttctcggt	60
gctgcccattg ctgagcagg accctacgaa ttctac	96

<210> 81

<211> 120

<212> DNA

<213> Homo sapiens

<400> 81

gtagaattcg taggggcccc caagctggcc cgctgcact acagcggcag catcaacgcc	60
tggagcacca aggagccctt cagctggatc aaggtggacc tgctggcccc catgatcatc	120

<210> 82

<211> 116

<212> DNA

<213> Homo sapiens

<400> 82

cacggcatca agaccaggg cgcccgccag aagttcagca gcctgtacat cagccagttc	60
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<210> 83

<211> 86

<212> DNA

<213> Homo sapiens

<400> 83

cggcacccctg atggtgttct tcggcaacgt ggacagcagc ggcatcaagc acaacatctt	60
caaccccccc gggctacaag ctttac	86

<210> 84

<211> 110

<212> DNA

<213> Homo sapiens

<400> 84

gtaaagcttg tagcccgggg ggggtgaaga tgttgtgctt gatgccgtg ctgtccacgt	60
tgccgaagaa caccatcagg gtgccggtgc tgttgccgcg gtaggtctgc	110

<210> 85

<211> 113

<212> DNA

<213> Homo sapiens

<400> 85

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ttctggcggg cgccctgggt cttgatgccg tggatgatca tggggggccag cag	113

<210> 86

<211> 99

<212> DNA

<213> Homo sapiens

<400> 86

gtccaccttg atccagctga agggctcctt ggtgctccag gcgttgatgc tgccgctgta	60
gtgcaggcgg gccagcttgg gggcccctac gaattctac	99

<210> 87

<211> 122

<212> DNA

<213> Homo sapiens

<400> 87

gtagaattcg taggatatca tcgcccgtta catccgctg cccccaccc actacagcat	60
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gg	122

<210> 88

<211> 112

<212> DNA

<213> Homo sapiens

<400> 88
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<210> 89
 <211> 89
 <212> DNA
 <213> Homo sapiens

<400> 89
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 gaccatgaag gtgaccctac aagctttac 89

<210> 90
 <211> 112
 <212> DNA
 <213> Homo sapiens

<400> 90
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 ggttggttac ctgggggccc caggcggttc tgcggccctg caggtgcagg cg 112

<210> 91
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 <212> DNA
 <213> Homo sapiens

<400> 91
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<210> 92
 <211> 97
 <212> DNA
 <213> Homo sapiens

<400> 92
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 gcggatgtag cgggcgatga tatcctacga attctac 97

<210> 93
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 <212> DNA
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<400> 93
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 tc 122

<210> 94
 <211> 104
 <212> DNA
 <213> Homo sapiens

<400> 94
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agcctggacc ccccccctgct gacccgctac ctgcgcatcc accc 104

<210> 95
 <211> 92
 <212> DNA
 <213> Homo sapiens

<400> 95
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 cctgtactag ctgcccgggc tacaagcttt ac 92

<210> 96
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 96
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 tgcgcagggc gatctggtgc acccagctct ggggggtggat gcgcaggtag cgggtcag 118

<210> 97
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 <212> DNA
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<400> 97
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<210> 98
 <211> 100
 <212> DNA
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<210> 99
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 <212> DNA
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 acatcagcgc ctacctgctg 140

<210> 100
 <211> 57
 <212> DNA
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<400> 100
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<210> 101

<211> 58
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<400> 101
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<210> 102
 <211> 79
 <212> DNA
 <213> Homo sapiens

<400> 102
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<210> 103
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 <212> DNA
 <213> Homo sapiens

<400> 103
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<210> 104
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 <212> DNA
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<400> 104
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<210> 105
 <211> 310
 <212> DNA
 <213> Artificial Sequence

<220>
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 gcgcttctgc ttcagcgcca ccgcgcgcta ctacctgggc gccgtggagc tgagctggga 120
 ctacatgcag agcgacctgg gcgagctgcc cgtggacgcc cgcttcccc ccgcgctgcc 180
 caagagcttc cccttcaaca ccagcgtggt gtacaagaag accctgttcg tggagtacac 240
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 caagctttac 310

<210> 106
 <211> 297
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

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 ccagcgaggg cgccgagtac gacgaccaga ccagccagcg cgagaaggag gacgacaagg 180
 tgttccccgg cggcagccac acctacgtgt ggcaggtgct gaaggagaac ggccccatgg 240
 ccagcgaccc cctgtgcctg acctacagct acctgagcca cgtgctacaa gctttac 297

<210> 107
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 107
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 tgatgcagga ccgcgacgcc gccagcgccc gcgcctggcc caagatgcac accgtgaacg 240
 gctacgtgaa ccgcagcctg cccggcctga tcggctgcca ccgcaagagc gtgtactggc 300
 acgtgctaca agctttac 318

<210> 108
 <211> 384
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 108
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 cacttctctg accgcccaga cctgctgat ggacctgggc cagtctctgc tgttctgcca 180
 catcagcagc caccagcacg acggcatgga ggcctacgtg aaggtggaca gctgcccga 240
 ggagccccag ctgcgcatga agaacaacga ggaggccgag gactacgacg acgacctgac 300
 cgacagcgag atggacgtgg tgcgcttcga cgacgacaac agccccagct tcatccagat 360
 ctctacggat cctacaagct ttac 384

<210> 109
 <211> 443
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 109
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 agctacaaga gccagtacct gaacaacggc cccagcgca tcggccgcaa gtacaagaag 180
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 agcggcatcc tgggccccct gctgtacggc gaggtgggag acaccctgct gatcatcttc 300
 aagaaccagg ccagccgccc ctacaacatc taccaccacg gcataccga cgtgcgcccc 360
 ctgtacagcc gccgcctgcc caaggcgctg aagcacctga aggacttccc catcctgccc 420
 ggcgagatct ctacaagctt tac 443

<210> 110
 <211> 266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

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 agggggccga tcaggccgct ggccaggctc cgctccatgt tcacgaagct gctgtagtag 180
 cgggtcaggc agcgggggtc gctcttggtg gggccgtcct ccacggtcac ggtccacttg 240
 tacttgaaga tctctacgaa ttctac 266

<210> 111
 <211> 341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 111
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 gtgttcgaca gctgacgct gagcgtgtgc ctgcacgagg tggcctactg gtacatcctg 180
 agcatcggcg ccagagccga cttcctgagc gtgttcttca gcggtacac cttcaagcac 240
 aagatgggtg acgaggacac cctgacctg ttccccttca gcggcgagac cgtgttcatg 300
 agcatggaga accccggcct gtggatccct acaagcttta c 341

<210> 112
 <211> 397
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

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 gaggacatca ggcctacct gctgagcaag aacaacgcca tcgagccccg cctggaggag 180
 atcacccgca ccacctgca gagcgaccag gaggagatcg actacgacga caccatcagc 240
 gtggagatga agaaggagga cttcgacatc tacgacgagg acgagaacca gagccccgc 300
 agcttccaga agaagaccg ccactacttc atcgccgcgc tggagcgccct gtgggactac 360
 ggcattgagca gcagccccca cgtgctacaa gctttac 397

<210> 113
 <211> 417
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 113
 gtagaattcg tagcacgtgc tgcgcaaccg cgcccagagc ggcagcgtgc cccagttcaa 60
 gaaggtggtg ttccaggagt tcaccgacgg cagcttcacc cagcccctgt accgcggcga 120
 gctgaacgag cacctggggc tgctggggcc ctacatccgc gccgaggtgg aggacaacat 180
 catggtgacc gtgcaggagt tcgccctggt cttcaccatc ttcgacgaga ccaagagctg 240
 gtacttcacc gagaacatgg agcgcaactg ccgcgcccc tgcaacatcc agatggagga 300
 cccaccttc aaggagaact accgcttcca cgccatcaac ggctacatca tggacaccct 360
 gcccggcctg gtgatggccc aggaccagcg catccgctgg taccctacaa gctttac 417

<210> 114
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 114
 gtagaattcg tagggtgacc ttccgcaacc aggccagccg cccctacagc ttctacagca 60
 gcctgatcag ctacgaggag gaccagcgcc agggcgccga gcccgcgaag aacttcgtga 120
 agcccaacga gaccaagacc tacttctgga aggtgcagca ccacatggcc cccaccaagg 180
 acgagttcga ctgcaaggcc tgggcctact tcagcgacgt ggacctggag aaggacgtgc 240
 acagcggcct gatcgggccc ctgctggtgt gccacaccaa caccctgaac cccgcccacg 300
 gccgccaggt gaccctacaa gctttac 327

<210> 115
 <211> 344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 115
 gtagaattcg tagggtacct gctgagcatg ggcagcaacg agaacatcca cagcatccac 60
 ttcagcggcc acgtgttcac cgtgcgcaag aaggaggagt acaagatggc cctgtacaac 120
 ctgtaccccc gcgtgttcga gaccgtggag atgctgcca gcaaggccgg catctggcgc 180
 gtggagtgcc tgatcggcga gcacctgcac gccggcatga gcacctggt cctggtgtac 240
 agcaacaagt gccagacccc cctgggcatg gccagcggcc acatccgcga cttccagatc 300
 accgccagcg gccagtagcg ccagtgggcc cctacaagct ttac 344

<210> 116
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 116
 gtagaattcg taggggcccc caagctggcc cgctgcact acagcggcag catcaacgcc 60
 tggagcacca aggagccctt cagctggatc aaggtggacc tgctggcccc catgatcacc 120
 cacggcatca agaccaggc cgcccgccag aagttcagca gcctgtacat cagccagttc 180
 atcatcatgt acagcctgga cggcaagaag tggcagacct accgcggcaa cagcaccggc 240
 accctgatgg tgttcttcgg caacgtggac agcagcggca tcaagcaca catcttcaac 300
 cccccgggc tacaagcttt ac 322

<210> 117
 <211> 323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 117
 gtagaattcg taggatatca tcgcccgcta catccgcctg caccaccacc actacagcat 60
 ccgcagcacc ctgcgcatgg agctgatggg ctgcgacctg aacagctgca gcatgccct 120
 gggcatggag agcaaggcca tcagcgacgc ccagatcacc gccagcagct acttcaccaa 180
 catgttcgcc acctggagcc ccagcaaggc ccgcctgcac ctgcagggcc gcagcaacgc 240
 ctggcgcccc caggtgaaca accccaagga gtggctgcag gtggacttcc agaagaccat 300
 gaaggtgacc ctacaagctt tac 323

<210> 118
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 118
 gtagaattcg tagggtgacc ggcgtgacca ccagggcgt gaagagcctg ctgaccagca 60
 tgtacgtgaa ggagttcctg atcagcagca gccaggacgg ccaccagtgg accctgttct 120
 tccagaacgg caaggtgaag gtgttccagg gcaaccagga cagcttcacc cccgtgggtga 180
 acagcctgga cccccccctg ctgacccgct acctgcgcac ccacccccag agctgggtgc 240
 accagatcgc cctgcgcgat gaggtgctgg gctgcgaggg ccaggacctg tactagctgc 300
 ccgggctaca agctttac 318

<210> 119
 <211> 310
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 119
 gtaaagcttg taggggcccc gcaggcccat ccaggggggg cggggcttgg cgatgttgaa 60
 caggtggctg gtgaactcca cgaacagggt cttcttgat accacgctgg tgttgaaggg 120
 gaagctcttg ggcacgcggg gggggaagcg ggcgtccacg ggcagctcgc ccaggtcgt 180
 ctgcatgtag tcccagctca gctccacggc gccaggtag tagcggcggg tggcgctgaa 240
 gcagaagcgc agcaggcaca ggaagaagca ggtgctcagc tcgatctgca tgctagccta 300
 cgaattctac 310

<210> 120
 <211> 297
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 120

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gtaaagcttg tagcacgtgg ctacaggtagc tgtaggtcag gcacaggggg tcgctggcca      60
tggggcccgtt ctcccttcagc acctgccaca cgtaggtgtg gctgccgccg gggaacacct      120
tgtcgctctc ctctctcgcg tggctggtct ggtcgctcgt ctcgccgccg tcgctggcct      180
tccagtagct caccgccacg gcgtgcaggc tcacggggtg gctggccatg ttcttcaggg      240
tgatcaccac ggtgtcgtac acctcggcct ggatggtggg gccctacga attctac          297

```

<210> 121
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

```

<400> 121
gtaaagcttg tagcacgtgc cagtacacgc tcttgccgtg gcagccgatc aggcggggca      60
ggctgcggtt cactagaccg ttacgggtgt gcattctggg ccaggccggg gcgctggcgg      120
cgctgcgggtc ctgcatcagg ctgttcttgg tctcgctgtg ccagctcttg cctcgtcga      180
acacggcgaa cagcaggatg aacttgtgca gggctctgggt cttctccttg gccaggctgc      240
cctcgcggca caccagcagg gcgccgatca ggccgctgtt caggtccttc accagggtcca      300
cgtggctacg aattctac

```

<210> 122
 <211> 384
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

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<400> 122
gtaaagcttg taggatccgt agagatctgg atgaagctgg ggctgttgtc gtcgtcgaag      60
cgcaccacgt ccattctcgt gtcggtcagg tcgtcgctgt agtcctcggc ctctcgttg      120
ttcttcatgc gcagctgggg ctctcggggg cagctgtcca ccttcacgta ggccctccatg      180
ccgtcgtgct ggtggctgct gatgtggcag aacagcagga actggcccag gtccatcagc      240
agggctctgg cggtcaggaa ggtgatgggg ctgatctcca ggctggcctg gcggtgggtg      300
cgcaccagga aggtgtggcc ctccaggaag atgctgtgca cctcgggggt ggtgcccatg      360
ccgatcacgt gctacgaatt ctac

```

<210> 123
 <211> 443
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

```

<400> 123
gtaaagcttg tagagatctc gccgggcagg atggggaagt ccttcagggtg cttcacgccc      60
ttgggcaggc ggcggctgta cagggggcgc acgtcggtga tgccgtgggg gtagatgttg      120
taggggcggc tggcctggtt cttgaagatg atcagcaggg tgctgcccac ctgcgcgtac      180
agcagggggc ccaggatgcc gctctcgtgc tggatggcct cgcgggtctt gaaggtctcg      240
tcggtgtagg ccatgaagcg caccttcttg tacttgccgc cgatgcgctg ggggcccgtt      300
ttcagggtact ggctcttgta gctgcggtcg tcgggggcca gcaccagggg ggcgtagtcc      360
cagtcctcct cctcggcggc gatgtagtgc acccagggtct tggggtgctt cttggccacg      420
ctgcggatcc ctacgaattc tac

```

<210> 124
 <211> 266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 124
 gtagaattcg tagagatctt caagtacaag tggaccgtga ccgtggagga cggccccacc 60
 aagagcgacc cccgctgcct gacccgctac tacagcagct tcgtgaacat ggagcgcgac 120
 ctggccagcg gcctgacgag cccctgctg atctgctaca aggagagcgt ggaccagcgc 180
 ggcaaccaga tcatgagcga caagcgcaac gtgatcctgt tcagcgtgtt cgacgagAAC 240
 cgcagctggt accctacaag ctttac 266

<210> 125
 <211> 341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 125
 gtaaagcttg tagggatcca caggccgggg ttctccatgc tcatgaacac ggtctcgccg 60
 ctgaagggga acagggtcag ggtgtcctcg tacaccatct tgtgcttgaa ggtgtagccg 120
 ctgaagaaca cgctcaggaa gtcgggtctgg gcgcccagtc tcaggatgta ccagtaggcc 180
 acctcgtgca ggcacacgct cagctgcagg ctgtcgaaca cgtagccgtt gatgctgtgc 240
 atgatgttgc tggcctggaa ctccgggtcc tccagctgca cgcggcgagg gttgggcagg 300
 aagcgttgga tgttctcggt cagggtaccct acgaattcta c 341

<210> 126
 <211> 397
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 126
 gtaaagcttg tagcacgtgg gggctgctgc tcatgccgta gtcccacagg cgctccacgg 60
 cggcgatgaa gtagtgccgg gtcttcttct ggaagctgcg ggggctctgg ttctcgtcct 120
 cgctcgtatg gtogaagtcc tccttcttca tctccacgct gatgggtgctg tcgtagtcga 180
 tctcctcctg gtcgctctgc aggggtggtgc ggggtgatctc ctccaggcgg ggctcgatgg 240
 cgttggttct gtcacagcag taggcgctga tgtcctcgta gctgtcctcg tagtagtcgc 300
 cgggtgttctt gtcgcagctg ctacacctca gcagggcggg catgccgcgg ttgcggaagt 360
 cgctgttgtg gcagcccagg atccctacga attctac 397

<210> 127
 <211> 417
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 127

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gtaaagcttg tagggtacca gcggatgcgc tggctctggg ccatcaccag gccgggcagg      60
gtgtccatga tgtagccgtt gatggcgtgg aagcggtagt tctccttgaa ggtgggggtcc    120
tccatctgga tgttgccagg ggcgcggcag ttgcgctcca tgttctcggg gaagtaccag    180
ctcttgggtct cgtcgaagat ggtgaagaac agggcgaact cctgcacggg caccatgatg    240
ttgtcctcca cctcggcgcg gatgtagggg cccagcaggc ccagggtgctc gttcagctcg    300
ccgcgggtaca ggggctgggt gaagctgccg tcgggtgaact cctggaacac caccttcttg    360
aactgggggca cgctgccgct ctgggcgcgg ttgcgcagca cgtgctacga attctac      417

```

<210> 128

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 128

```

gtaaagcttg tagggtcacc tggcggccgt gggcgggggt caggggtgttg gtgtggcaca      60
ccagcagggg gccgatcagg ccgctgtgca cgtccttctc cagggtccacg tcgctgaagt    120
aggcccaggc cttgcagtcg aactcgtcct tgggtggggg catgtgggtgc tgcaccttcc    180
agaagtaggt cttgggtctcg ttgggcttca cgaagtctct gcggggctcg gcgccctggc    240
gctgggtcctc ctcgtagctg atcaggctgc tgtagaagct gtaggggcgg ctggcctggg    300
tgcggaaggt caccctacga attctac      327

```

<210> 129

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 129

```

gtaaagcttg taggggcccc ctggccgtac tggccgctgg cgggtgatctg gaagtgcggg      60
atgtggccgc tggccatgcc caggggggtc tggcacttgt tgctgtacac caggaacagg    120
gtgctcatgc cggcgtgcag gtgctcgccg atcaggcact ccacgcgcca gatgccggcc    180
ttgctgggca gcatctccac ggtctcgaac acgcgggggt acaggttgta cagggccatc    240
ttgtactcct ccttcttgcg cacggtgaac acgtggccgc tgaagtggat gctgtggatg    300
ttctcgtttg tgcccatgct cagcagggtac cctacgaatt ctac      344

```

<210> 130

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 130

```

gtaaagcttg tagcccgggg ggggtgaaga tgttgtgctt gatgccgctg ctgtccacgt      60
tgccgaagaa caccatcagg gtgccggtgc tgttgccgcg gtaggtctgc cacttcttgc    120
cgtccaggct gtacatgatg atgaactggc tgatgtacag gctgctgaac ttctggcggg    180
cgccctgggt cttgatgccg tggatgatca tggggggccag cagggtccacc ttgatccagc    240
tgaagggctc cttgggtgctc caggcggtga tgctgccgct gtagtgccagg cggggccagct    300
tggggggcccc tacgaattct ac      322

```

<210> 131

<211> 323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 131
 gtaaagcttg tagggtcacc ttcattggtct tctggaagtc cacctgcagc cactccttgg 60
 ggttggtcac ctggggggcgc caggcgttgc tgcggccctg cagggtgcagg cgggccttgc 120
 tggggctcca ggtggcgaac atgttggtga agtagctgct ggcggtgatc tgggcgtcgc 180
 tgatggcctt gctctccatg ccaggggca tgcctgcagct gttcaggctc cagcccatca 240
 gctccatgcg cagggtgctg cggatgctgt agtgggtggg gtgcaggcgg atgtagcggg 300
 cgatgatatc ctacgaattc tac 323

<210> 132
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 132
 gtaaagcttg tagcccgggc agctagtaca ggtcctgggc ctgcagccc agcacctcca 60
 tgcgcagggc gatctggtgc acccagctct gggggtggat gcgcaggtag cgggtcagca 120
 gggggggggtc caggctgttc accacggggg tgaagctgtc ctgggtgccc tggaacacct 180
 tcaccttgcc gttctggaag aacagggtcc actggtggcc gtccctggctg ctgctgatca 240
 ggaactcctt caggtacatg ctggtcagca ggctcttcac gccctgggtg gtcacgcggg 300
 tcacctacg aattctac 318

<210> 133
 <211> 255
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 133
 gtagaattcg gatcctgggc tgccacaaca ggcacttccg caaccggggc atgaccgccc 60
 tgctgaaggt gagcagctgc gacaagaaca ccggcgacta ctacgaggac agctacgagg 120
 acatcagcgc ctacctgctg agcaagaaca acgccatcga gccccgcagg cgcaggcgcg 180
 agatcaccgc caccacctg cagagcgacc aggaggagat cgactacgac gacaccatca 240
 gcgtggaagc ttac 255

<210> 134
 <211> 255
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated construct

<400> 134
 gtaaagcttc cacgctgatg gtgtcgtcgt agtcgatctc ctccctggctg ctctgcaggg 60
 tgggtgcgggt gatctcgcgc ctgcgcctgc ggggctcgat ggcgttggtc ttgctcagca 120

ggtaggcgct gatgtcctcg tagctgtcct cgtagtagtc gccggtgttc ttgtcgcagc	180
tgctcacctt cagcagggcg gtcatgccgc ggttgcgga gtcgctgttg tggcagccca	240
ggatccgaat tctac	255

<210> 135

<211> 4

<212> PRT

<213> Homo sapiens

<400> 135

Arg Arg Arg Arg

1

<210> 136

<211> 5

<212> PRT

<213> Homo sapiens

<400> 136

Arg Arg Arg Arg Arg

1

5